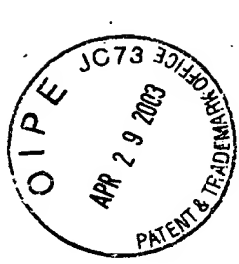


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1 AAGCTTTCCT GATCTCTAAA TCAAGGTCAG CTCCCTAAGC TCTTGGCTCC
51 CGTACTGAAA CTTTTTCTTA TGTAAGTCTC ATAAACACAT AGCATAATGT
101 TTTGCATGTT TTTCTTCCCT ATCAGTTGCA AGTTCCAGCA GAGCTGATAT
151 ATTTTCATTT CATTGCTAC TATAGCCCTA GAGCCTGACA TAGTTTCTGG
201 CTGTGAATGC TCAATAAATA TTTGTTTAAT TGAGTAGAAA CATAAAGTAT
251 CTATTTTCATT GAAGGAAAGA ATAATTAGCT ACATTTTTCT TTTTCTTGCC
301 TTAATATTTG AGGAATTTGC TTATATGTCA TAATAAAAAA GTTAAAGCCT
351 TATACATTAT ACTAAGGAAT TTGGACATTA AATTCAAGCT AGCCTTTCTA
401 TAAACAAAAT ACTGAATTTT TGTCCCTAAA TTTGTTTCCT CCCTATTCTT
451 CCCCATTGAG ATGACACCAA ATCCCTCTAG CTGCTCAAAC CAAGTACCCG
501 TATGTTATTC TTAATTATCT CTTTACCTTG CTTCTCATAT GCAATTTGTT
551 AACAAGTCAT CTTGAGTCTG TATCCATTAT TCTCCCTTTC CAGACCACCA
601 ACATGTCTTG ACTATACTGC TACAATAGCC TCCCAACTCT TGTCCTACTT
651 AAAATTCATT GTAAAAATC AGTCTTGGCC GGGCAGGTG GCTCACACCT
701 ATAATCCCAG CACTTTGGGA GTCCCAGGCG GGCGGGTCAC GAGGTCAAGA
751 GATGGAGACC ATCATGGCCA ACATGGTGAA ACCCTGTCTC TACTATAAAT
801 ACAAAAAAAT TATCTGGGTG TGGTGGCACA TGCCTGTAAT CCCAACTACT
851 AGGGAGGCTG AGGCAGGAGA ATCGCTTGAA CCTGGGAGGC GGAGGTTGCA
901 GTGAGCCGAG ATCGCACCAT TGCACCTCAG CCTGGCAACA GACGAGACT
951 CCATCCCCAA ACAAACAAA ACAAACCAT GTAAAACATG TCTGTAAAAC
1,001 ATGTCAGATT TCGTGTTTCA AAGTCTTACA TGTCTTTTCA TTATGCTAAG
1,051 ATAAAACCCA AATGCATTTT CTTGGTTTCT AAAGCCAAGA AAATAAGAGT
1,101 TGCTTTCAGC AACCTTGTTT CTTCCGCCAT GCTTTTCCCT AGCTCACTCT
1,151 TTTTAGGCAA GTCGACCTGA TTTTCTTTCT GTTAGTCTGT TTCTGCCTCG
1,201 TGGTCTGGCT TTCTTTCTGT TAGTCTGTTT CCACCTCGTG GTCTTGGTCC
1,251 TGGCTCTTCA TTCTGCCTGG AATGCTCTCC ACTCCAGATC CTTACTAGAT
1,301 CTTAGCTCAG TCATCACCTT CGCAGGAAGA TCTTCCAACC ATTCACCTGC
1,351 ATACACCTAT GGCTGCTCCC TAGAGAACAT CATTCTGTTT TCTTCACTTC
1,401 CTAGCACTTA CTGCTTTCTG AAATTATCTA CTTTGATTGT TTATTTCTTT
1,451 CTTTACTCTT ACTAGGATAC CTGGGTCATT AAAGGAGGGA TATTTCTCTC
1,501 TTATTTACTG TTATAAACTT AATGCTTAGG CTGTAGAAGT TATACAATAT
1,551 TTGAAGAATA AATCGTTAAA TGTATAACAT TTTTGAAGAA AGATAATTGT

FIG. 2



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FIG. 2 - Continued

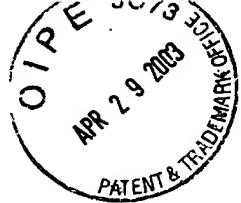
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1,651 ATGGTAAAGG ACAAAGACAT ATTTTATAGG ACTGTACCCT GAAAAATAAA
1,701 TAAACTTGAA CCAGTTATAC AAGACTTATG TGCAGGAAAC AGGTACCAGT
1,751 TATATTTAGA AATGGTAAAT CACCTTCTAA GCATAACTCA GAGCACAATA
1,801 TATTAGAGGG TAGAGAGAGA AGTGCGTCTT AGATATTGGT AATCATATTA
1,851 GGACTGACGC CATCCTTGAT TTTTCTTCTG GGAAACAGCT CAAAATGACT
1,901 ATTTAATGTT TACAATGATA TCTTGCATCT TGCCAGTAAA TAATATAATA
1,951 GACACTAGGA ATCCAAATTG TAAGATGAAC AAGTCTTTAT AGAGGGAGAG
2,001 CCAAATACAC AATAAATAAC ACAAGGTGGT AAATGCAGTA ATACAAACAT
2,051 ACATACCATG CATAGGAGTG CAGAGAAGGT GTGCTTCTCC GAATGCAGTC
2,101 ACCCAGAAAG TCCTTCTGTA GAAAGGGATA TCTTAAATGG TCCTTAAAGG
2,151 AAAAGTAACC AAAGGCAACT AAAGATTGCA AGGAGGTCCC AGGAAAAAGC
2,201 AAAAGAACCA AAGGTACATA GGCACAAAAG TAGCCTGCCT TCCTGGGAAC
2,251 TTCCAATAGT TTGCTGGAGC ACACAGTTAG AAGTACTGTG CCATGGGAGC
2,301 AAAGACTGAA GACATATGCA GGTTCAAGGG CACAGAGCCC CATATATGTC
2,351 ATGATAAGAT ATTGGGAAGC CACTGGGGAG CTACTGAAAC TTTAAGCAGG
2,401 GAAATAAAAT TGTCATATCT ACACCTTAGA AATTTGATTT TTTTCTCTTC
2,451 TTTTATCTTC TCTTCTCCTC TCTTCTCTCT CTCTCTCTCT CTCTCTCTCT
2,501 GTGTGTGTGT GTGTGTGTGT GTGTGTGTGT GACAGAGTCC TGCTCTGTCA
2,551 CCCAGGCTGG AGTGTAGTGG AGTGATCTCC GCTTACTGCA GTCTCTGCCT
2,601 CTCAAGCGAT TCCCTGCCTC AGCCTCCCGA GTAGCTGGGA TTACAGGCGG
2,651 GCTCTACAAC AGCTGGCTAA CTTTTGTATT TTTTGGTAAC AACCAGGTTT
2,701 TACCATGTTG GCCAGGCTGG TCTTGAAGTC CTGACCTCAG GTGATCTGCC
2,751 TGCCTTGGCT TTCCAAAGTG CTGGGATTAC AGGCGTGAGC CACCCTGCCT
2,801 GGTGTAGAAG TTTGATTTTG ATGTCAGTGT GGTAGATGAA TTTGTGGGAA
2,851 GCAAAACAAG ATAGAGTTCA ATGACAGTGA AAAGTTTATT GTATAAGCTA
2,901 TATAAAAGAA AATGTTGAAG GTTTGAAATC CATTAGTGGC AGTAAGGGTG
2,951 TACAGAACGA AACTATTTGA GAAGTACACA AGGCAAGTCT TACTTTCAAG
3,001 GCAGTTTATG TAAGCTCATT CAATTGTCTC AGTGTTCTTG CTATGTGTGG
3,051 GTTATAGGAT TTGGAACATA TGATCAATCT GAGCACACAT CAGTAACTG
3,101 AATAGGATTA TTAAAATCCA CAAGCATTTT ACTAGTGGAA TCTGTGATAT
3,151 TTTCTAGCTA CTCTTGCTTG TTTTATTTGA ATCTTTTGCT CATATCCTAT
3,201 AGTAAAGATT TCAGGAAATA TATTTTTATT TGCCTAGAAT TTTAGCCTTT



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FIG. 2 - Continued

3,251	TAGTTTTTTG	AATCTATTGC	TCATATTCTT	ATAGTAAGAG	TTTCAGGGAA
3,301	TGTATTTCTA	TTTGTCTGGA	ATTTTAGCCT	TTCAGGTTTT	TGAGCCCCTC
3,351	TTTTGCTTAT	GGGACATAGT	ATGAGACAAG	ATGAAATGAT	ACTTCTATTC
3,401	CCAATTCACT	GATGGGGAAA	ATGAAGCAAA	AAATGTTATT	CACTCAAGGC
3,451	TTCTGCCATG	TTTCCTGGTG	GAATTACGGC	TCAGACACAA	ATTCCTAAT
3,501	GCCTGTGCTG	CTAACTTCTC	AATAGAACAC	TATATTAATT	TATCTTCTTC
3,551	CTGAGTGTTT	TTCCACAAAT	CCCATAGCCT	GTGAAAAGAT	TGTTTTAGGG
3,601	AAATATTATT	TTTAATATAG	CATATTTTGT	CAATGTGGGA	CATAGGACTA
3,651	GTACCTGCTG	AAAACCATCT	CATGATCCTT	GTGTAAGAAC	TAATTCACAC
3,701	TAGAAATACT	ATTTTCCTTG	CTCATTAATA	ACATAAATGT	CTCAGAAAGT
3,751	AAAAAATTAT	TCCTCTCTAA	ATAAACATAC	ATGCCACTCA	AATTTTATTC
3,801	CTCTACCACT	TGCCGTATCT	AAACCTAGTT	AGATACTTTG	GTTTTAGGTA
3,851	TAATCTGACA	GAACAGATAC	AACCAAGATC	ACATTGTGAG	TCAGAAGTGG
3,901	AAAATTCATA	ATTCATGATG	ATACCAATAA	AAGATAGATT	TAGCTTTTTA
3,951	CAGGATGTTT	TTGGCATTTC	ATTCTTTCAT	TTGAGGGGAG	ATCTCACCAA
4,001	AATATGTCTT	TCATGGTTCA	TTGTGTTATT	TAATTTCTGT	GATGCATATT
4,051	CTCAGGTTAC	TTTAAACCTA	GTCTATAGAT	TCAAAGATAT	CCCGTGTCAG
4,101	GTCTCTAAAA	GTAAAAAGAA	AAATGGGTAC	TTGTGAAGGC	TGATTCACAG
4,151	TAAGTAGTGT	AGAGGGGAGT	GCCTTGTGTA	TTCACAAATT	ATCAACGTGA
4,201	GCATCAGATA	AGATTTTCTT	TAGTCACACA	CACCTACCTT	CTTACTAGGA
4,251	AGATCCATAT	ACTTGAATAA	TTGTTCTGCT	TGACCCAGGT	TACTTATCAG
4,301	TCCCTTTATT	ATAATATTTG	TAAATATTGG	GGCTCGAGAA	CCGAGCGGAG
4,351	CTGGTTGAGT	CTTCAAAGTC	CTAAAACGTG	CGGCCGTGGG	TTTCGAGGTTT
4,401	ATTGATTGAA	TTCGGCTGGC	ACGAGAGCCT	CTGCAGACAG	AGAGCGCGAG
4,451	AGATGGAGAT	GGGCAGACGG	ATTCATTTCAG	AGCTGCGGAA	CAGGGCGCCC
4,501	TCTGATGTGA	AAGAACTTGC	CCTGGACAAC	AGTCGGTCGA	ATGAAGGCAA
4,551	ACTCGAAGCC	CTCACAGATG	AATTTGAAGA	ACTGGAATTC	TTAAGTAAAA
4,601	TCAACGGAGG	CCTCACCTCA	ATCTCAGACT	TACCAAAGTT	AAAGTTGAGA
4,651	AAGCTTGAAC	TAAGAGTCTC	AGGGGGCCTG	GAAGTATTGG	CAGAAAAGTG
4,701	TCCAAACCTC	ACGCATCTAT	ATTTAAGTGG	CAACAAAATT	AAAGACCTCA
4,751	GCACAATAGA	GCCACTGAAA	CAGTTAGAAA	ACCTCAAGAG	CTTAGACCTT
4,801	TTCAATTGCG	AGGTAACCAA	CCTGAACGAC	TACGGAGAAA	ACGTGTTCAA
4,851	GCTTCTCCTG	CAACTCACAT	ATCTCGACAG	CTGTTACTGG	GACCACAAGG
4,901	AGGCCCTTA	CTCAGATATT	GAGGACCACG	TGGAGGGCCT	GGATGACGAG



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FIG. 2 - Continued

4,951 GAGGAGGGTG AGCATGAGGA GGAGTATGAT GAAGATGCTC AGGTAGTGGA
5,001 AGATGAGGAG GCGGAGGAGG AGGAGGAGGA AGGTGAAGAG GAGGACGTGA
5,051 GTGGAGGGGA CGAGGAGGAT GAAGAAGGTT ATAACGATGG AGAGGTAGAT
5,101 GCGGAGGAAG ATGAAGAAGA GCTTGGTGAA GAAGAAAGGG GTCAGAAGCG
5,151 AAAATGAGAA CCTGAAGATG AGGGAGAAGA TGATGACTAA GTAGAATAAC
5,201 CTATTTTGAA AAATTCCTAT TGTGATTTGA CTGTTTTTTAC CCATATCCCC
5,251 TCCCCCTCC AATCCTGCCC CCTGAAACTT ACTTTTTTCT GATTGTAACA
5,301 TTGCTGTGGG AATGAGACGG GAAAAGTGTA CTGGGGGTTG TGGAGGGAGG
5,351 GAGGGCAGGA GCGGGTGGAC TAAAATACTA TTTTACTGTC CAAATAAAAT
5,401 AATATTTGTA AATATTAAC TGGATACTAG CTTTGTAGAA TGATTACTAT
5,451 TAATTATTCT CTCTCTCTTT TTATTTTTTT ACACATTCTA TTCTTTTAAG
5,501 TATAGTCCTT TTAGTCCAAG GAAAAGGCAC TACAATCCAC TTATTAATGC
5,551 TTGCTACTGT GTTCAAGTAA AATAAGCTCC AGGATTTAAC AAAAGAGGA
5,601 AAGAAAATAT TTACAATGAA AATGTTGCTA AAAATTTAAA ACAAATTACA
5,651 GTAAATGTAT TGTAAAGCA AATTCTATTT TTAAAATTTA TTAATAAGGA
5,701 AATAATTTGC TAAAGCAAAT TTTTGAAAA ATAATAATGC ACTTTATACT
5,751 TGATTTTATT TATTAAACA ATGATTTATA AGCTT (SEQ ID NO: 1)



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4,357 GAGTCTTCAA AGTCCTAAAA CGTGGCGCCG TGGGTTCGAG GTTTATTGAT TGAATTCGGC
1 gaattcccaa agtcctaaaa cgcgcgccg tgggttcggg gtttattgat tgaattccgc

4,417 TGGC³CGAGA GCCTCTGCAG ACAGAGAGCG CGAGAGATGG AGATGGGCAG ACGGATTCAT
61 cgcgcgcgga gcctctgcag agagagagcg cgagagatgg agatgggcag acggattcat

4,477 TCAGAGCTGC GGAACAGGGC GCCCTCTGAT GTGAAAGAAC TTGCCCTGGA CAACAGTCGG
121 ttagagctgc ggaacaggac gccctctgat gtgaaagaac ttgtcctgga caacagtcgg

4,537 TCGAATGAAG GCAA³ACTCGA AGCCCTCACA GATGAATTTG AAGAACTGGA ATTCTTAAGT
181 tcgaatgaag gcaaactcga aggccctaca gatgaatttg aagaactgga attctttaagt

4,597 AAAATCAACG GAGGCCTCAC CTCAATCTCA GACTTACCAA AGTTAAAGTT GAGA---AAG
241 acaatcaacg taggcctcac ctcaatcgca aacttaccaa agttaacaa acttaagaag

4,654 CTTGAACTAA -----G AGTCTCAGGG GGCCTGGAAG TATTGGCAGA AAAGTGTCCA
301 cttgaactaa gcgataacag agtctcaggg ggcctagaag tattggcaga aaagtgtccg

4,705 AACCTCACGC ATCTATATTT AAGTGGCAAC AAAATTAAAG ACCTCAGCAC AATAGAGCCA
361 aacctcacgc atctaaattt aagtggcaac aaaattaaag acctcagcac aatagagcca

4,765 CTGAAACAGT TAGAAAACCT CAAGAGCTTA GACCTTTTCA ATTGCGAGGT AACCAACCTG
421 ctgaaaaagt tagaaaacct caagagctta gaccttttca attgcgaggt aaccaacctg

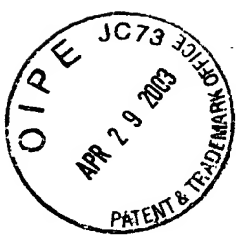
4,825 AACGACTACG GAGAAAACGT GTTCAAGCTT CTCCTGCAAC TCACATATCT CGACAGCTGT
481 aacgactacc gagaaaatgt gttcaagctc ctcccgaac tcacatatct cgacggctat

4,885 TACTGGGACC ACAAGGAGGC CCCTTACTCA GATATTGAGG ACCACGTGGA GGGCCTGGAT
541 gaccgggacg acaaggaggc ccctgactcg gatgctgagg gctacgtgga gggcctggat

4,945 GACGAGGAGG AGGGTGAGCA TGAGGAGGAG TATGATGAAG ATGCTCAGGT AGTGGAAGAT
601 gatgaggagg aggatgagga tgaggaggag tatgatgaag atgctcaggt agtggaagac

5,005 GAGGAGGGCG AGGAGGAGGA GGAGGAAGGT GAAGAGGAGG ACGTGAGTGG AGGGGACGAG
661 gaggaggacg aggatgagga ggaggaaggt gaagaggagg acgtgagtgg agaggaggag

FIG. 3



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FIG. 3 - Continued

5,065 GAGGATGAAG AAGGTTATAA CGATGGAGAG GTAGATGGCG AGGAAGATGA AGAAGAGCTT
721 gaggatgaag aaggttataa cgatggagag gtagatgacg aggaagatga agaagagctt

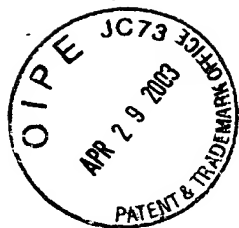
5,125 GGTGAAGAAG AAAGGGGTCA GAAGCGAAAA TGAGAACCTG AAGATGAGGC AGAAGATGAT
781 ggtgaagaag aaaggggtca gaagcgaaaa cgagaacctg aagatgaggg agaagatgat

5,185 GACTAAGTAG AATAACCTAT TTTGAAAAAT TCCTATTGTG ATTTGACTGT TTTTACCCAT
841 gactaagtgg aataacctat ttgaaaaat tcctattgtg atttgactgt ttttaccat

5,245 ATCCCCTCCC CCCTCC---- --AATCCTGC CCCCTGAAAC TTACTTTTTT CTGATTGTAA
901 atcccctctc cccccccct ctaatcctgc cccctgaaac ttattttttt ctgattgtaa

5,299 CATTGCTGTG GGAATGAGAC GGGAAAAGTG TACTGGGGGT TGTGGAGGGA GGGAGGGCAG
961 cgttgctgtg ggaacgagag gggaagagtg tactgggggt tgcgggggga ggatggcggg

5,359 GAGGCGGTGG ACTAAAATAC TATTTTACT GCC (SEQ ID NO: 2)
1,021 tggg-ggtgg aataaaatac tatttttact gcc (SEQ ID NO: 3)



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1 MEMGRRIHSE LRNRAPSDVK ELALDNSRSN EGKLEALTDE
1 MEMGRRIHLE LRNRTPSDVK ELVLDNSRSN EGKLEGLTDE

41 FEELEFLSKI NGGLTSISDL PKL-KLRKLE L---RVSGGL
41 FEELEFLSTI NVGLTSIANL PKLNKLEKLE LSDNRVSGGL

77 EVLAEKCPNL THLYLSGNKI KDLSTIEPLK QLENLKSLDL
81 EVLAEKCPNL THLNLSGNKI KDLSTIEPLK KLENLKSLDL

117 FNCEVTNLND YGENVFKLLL QLT~~Y~~LDSCYW DHKEAPYSDI
121 FNCEVTNLND YRENVFKLLP QLT~~Y~~LDGYDR DDKEAPSDA

157 EDHVEGLDDE EGEHEEEYD EDAQVVEDEE GEEEEEEGEE
161 EGYVEGLDDE EDEDEEEYD EDAQVVEDEE DEEEEEEGEE

197 EDVSGGDEED EEGYNDGEVD GEEDEEEELGE EERGQKRK*-
201 EDVSGEEEEED EEGYNDGEVD DEEDEEEELGE EERGQKRKRE

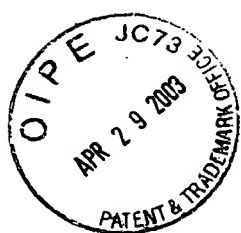
----- (SEQ ID NO: 4)
241 PEDEGEDDD* (SEQ ID NO: 5)

FIG. 4

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...
GGGTTCGAGGTTTATTGATTGAATTCGGCTGGCACGAGAGCCTCTGCAGACA
GAGAGCGCGAGAGATGGAGATGGGCAGACGGATTCATTCAGAGCTGCGGAA
CAGGGCGCCCTCTGATCTGAAAGAACTTGCCCTGGACAACAGTCGGTCGAA
TGAAGGCAAACTCGAAGCCCTCACAGATGAATTTGAAGAACTGGAATTCTT
AAGTAAAATCAACGGAGGCCTCACCTCAATCTCAGACTTACCAAAGTTAAA
GTTGAGAAAGCTTGAACCTAAGAGTCTCAGGGGGCCTGGAAGTATTGGCAGA
AAAGTGTCCAAACCTCACGCATCTATATTTAAGTGGCAACAAAATTAAAGA
CCTCAGCACAATAGAGCCACTGAAACAGTTAGAAAACCTCAAGAGCTTAGA
CCTTTTCAATTGCCAGGTAACCAACCTGAACGACTACGGAGAAAACGTGTTC
AAGCTTCTCCTGCAACTCACATATCTCGACAGCTGTTACTGGGACCACAAGG
AGCCCCCTTACTCAGATATTGAGGACCACGTGGAGGGCCTGGATGACGAGG
AGCAGGGTGAGCATGAGGAGGAGTATGATGAAGATGCTCAGGTAGTGGAAG
ATGAGGAGGGCGAGGAGGAGGAGGAAGGTGAAGAGGAGGACGTGAGT
GGAGGGGACCAGGAGGATGAAGAAGGTTATAACGATGGAGAGCTAGATGG
CGAGGAAGATGAAGAAGAGCTTGGTGAAGAAGAAAGGGGTCAGAAGCGAA
AATGAGAACCTGAAGATGAGGGAGAAGATGATGACTAAGTAGAATAACCTA
TTTGTAAAAATTCTATTGTGATTTGACTGTTTTTACCCATATCCCCCTCCCC
CTCCAATCCTGCCCCCTGAA (SEQ ID NO: 6)

FIG. 5



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50

1

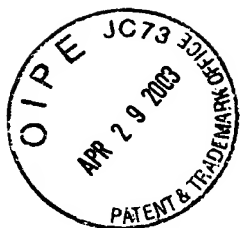
hnp32			c		
AF008216	a		g	a	a
TSU6			g		
TSU3			g	a	a
TSU1		g		t	a
P8			c		
P3		g		t	a
L3			c		
FT3-3			g	a	a
FT3-18		g		t	a
FT2-4		g		t	a
FT2-2			g	a	a
FT1-7			c		
FT1-3			c		
FT1-11		g		t	a
D5			c		
D3			c		
D1			c		
Consensus	GGGTTCGGGG	TTTATTGATT	GAATTCCGCT	GGCGCGGGAG	CCTCTGCAGA

100

51

hnp32						c
AF008216	c					
TSU6						c
TSU3	c			c		
TSU1		a	t		a	t
P8						
P3		a	c	...	t	
L3						
FT3-3	c					c
FT3-18		a	t		a	t
FT2-4		a	t		a	t
FT2-2	c					c
FT1-7		g				
FT1-3						
FT1-11		a	t		a	t
D5						c
D3						
D1				g		
Consensus	GAGAGAGCGC	-GAGAGATGG	AGATGGGCAG	ACGGATTTCAT	TTAGAGCTGC	

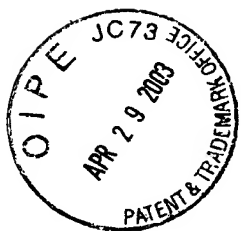
FIG. 7A



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FIG. 7A - Continued

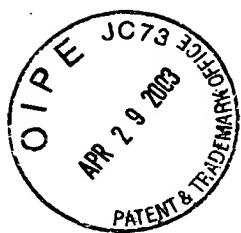
	101					150
hpp32					c	
AF008216		g				
TSU6	g				c	
TSU3		g			t	a
TSU1			c			
P8					t	a
P3			c			
L3						
FT3-3		g			c	
FT3-18			c		t	a
FT2-4			c		t	a
FT2-2		g				
FT1-7						
FT1-3					t	a
FT1-11			c			
D5					t	
D3						
D1						
Consensus	GGAACAGGAC GCCCTCTGAT GTGAAAGAAC TTGTCCTGGA CAACAGTCGG					
	151					200
hpp32					c	
AF008216						
TSU6					c	
TSU3						
TSU1	a		t g			
P8						
P3	a		t g			
L3					c	
FT3-3						g
FT3-18	a		t g			
FT2-4	a		t g			
FT2-2					c	
FT1-7						
FT1-3				g		
FT1-11	a		t g			
D5						
D3						
D1						
Consensus	TCGAATGAAG GCAAACTCGA AGGCCTCACA GATGAATTTG AAGAACTGGA					



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FIG. 7A - Continued

	201				250
hpb32					
AF008216		a	g	t	g
TSU6					
TSU3		a	g	t	g
TSU1	a	a	a	t	g
P8					g
P3	a	a	a	t	g
L3					
FT3-3		a	g	t	g
FT3-18	a	a	a	t	g
FT2-1	a	a	a	t	g
FT2-2		a	g	t	g
FT1-7					
FT1-3					
FT1-11	a	a	a	t	g
D5					
D3					
D1					
Consensus	ATTCTTAAGT ACAATCAACG TAGGCCTCAC CTCAATCGCA AACTTACCAA				
	251				300
hpb32				ga	
AF008216	...	gt g ga	c	t
TSU6					
TSU3	...	gt g ga	c	t
TSU1				c	t
P8				c	t
P3					
L3				ga	
FT3-3	...	gt g ga	c	t
FT3-18				c	t
FT2-4					
FT2-2	...	gt g ga a		
FT1-7	...	gt g ga		
FT1-3			ga		
FT1-11				c	t
D5			ga		
D3			ga		
D1			ga		
Consensus	AGTTAAACAA ACTTAAGAAG CTTGAACTAA GCAGTAACAG AGTCTCAGGG				

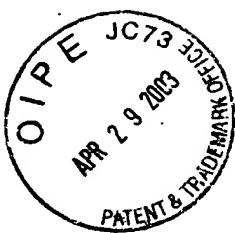


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FIG. 7A - Continued

	301			350
hpp32		g		t
AF008216	g		ta	
TSU6				t
TSU3	g		ta	
TSU1			ta	
P8			ta	
P3			ta	
L3	g	g		t
FT3-3	g		ta	
FT3-18			ta	
FT2-4				t
FT2-2	g			c t
FT1-7	g			
FT1-3	g	g	ta	
FT1-11		g		
D5			ta	
D3				
D1	g	g		
Consensus	GGCCTAGAAG	TATTGGCAGA	AAAGTGTCCA	AACCTCACGC ATCTAAATTT

	351			400
hpp32				c
AF008216			c	
TSU6				c
TSU3			c	
TSU1				
P8			c	
P3				
L3				c
FT3-3			c	
FT3-18			c	
FT2-4				c
FT2-2				c
FT1-7				
FT1-3			c	
FT1-11				
D5			c	
D3				
D1				
Consensus	AAGTGCCAAC	AAAATTAAAG	ACCTCAGCAC	AATAGAGCCA CTGAAAAAGT

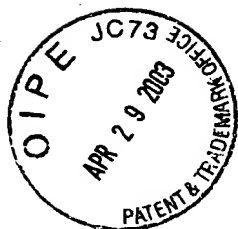


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FIG. 7A - Continued

401
hpp32
AF008216
TSU6 g c
TSU3 c
TSU1 c
P8 c
P3 g c
L3
FT3-3
FT3-18 g c
FT2-4 g c
FT2-2
FT1-7
FT1-3 c
FT1-11 g c
D5 c
D3 g
D1
Consensus TAGAAAACCT CAAGAGCTTA GACCTTTTCA ATTGCGAGGT AACCAACCTG

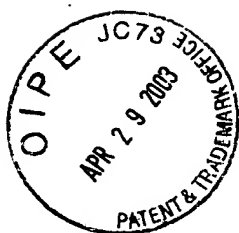
451
hpp32 c
AF008216 g c t
TSU6 a t g ga t
TSU3 g c
TSU1 a t ga
P8 c
P3 a c
L3 c
FT3-3 g c t
FT3-18 a t ga
FT2-4 a t ga
FT2-2 g c t
FT1-7 g c t
FT1-3 c
FT1-11 a t ga c
D5 c
D3 a t ga
D1 c
Consensus AACGACTACC GAGAAAATGT GTTCAAGCTC CTCCTGCAAC TCACATATCT



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FIG. 7A - Continued

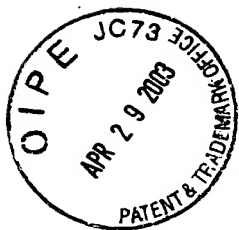
	501							550
hnp32		a						
AF008216		a	t	c		t	a	at
TSU6	a		c	t		a		g
TSU3	a	t	t	c		t	a	at
TSU1	a		c	t		a		g
P8		a						
P3		a						
L3		a						
FT3-3		a	t	t	c	t	a	at
FT3-18	a		c	t		a		g
FT2-4	a		c	t		a		g
FT2-2		a	t	c		t	a	at
FT1-7		a	t	c		t	a	at
FT1-3		a						
FT1-11	a		c	t		a		g
D5		a						
D3	a		c	t		a		g
D1		a						
Consensus	CGACGGCTGT	GACCGGGACG	ACAAGGAGGC	CCCTGACTCG	GATGCTGAGG			
	551							600
hnp32					t			
AF008216	a c					g	c	
TSU6	tt	t		a				
TSU3	c c					g	c	
TSU1	tt	t		a				
P8				t				
P3				t				
L3				t				
FT3-3	a c					g	c	
FT3-18			c	t				
FT2-4	tt	t		a				
FT2-2	a c					g	c	
FT1-7	a c					g	c	
FT1-3				t				
FT1-11	tt	t		a				
D5				t				
D3	tt	t		a				
D1				t				
Consensus	GCTACCTGGA	GGGCCTGGAT	GACGAGGAGG	AGGATGAGGA	TGAGGAGGAG			



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FIG. 7A - Continued

	601			650
hnp32			c	
AF008216				g g
TSU6		a		
TSU3				g g
TSU1		a		
P8		a	c	
P3			c	
L3			c	
FT3-3				g g
FT3-18			c	
FT2-4		a		
FT2-2				g g
FT1-7				g g g
FT1-3			c	
FT1-11		a		
D5			c	
D3		a		
D1			c	
Consensus	TATGATGAAG	ATGCTCAGGT	AGTGGAAAGAT	GAGGAGGACG AGGATGAGGA
	651			700
hnp32				
AF008216			g c	
TSU6	c		c	a g t
TSU3			g c	
TSU1	c		c	a g t
P8				
P3				
L3				
FT3-3			g c g	
FT3-18				
FT2-4	c		c	a g t
FT2-2			g c	
FT1-7			g c	
FT1-3				
FT1-11	c		c	a g t
D5				
D3	c		c	a g t
D1				
Consensus	GGAGGAAGGT	GAAGAGGAGG	ACGTGAGTGG	AGAGGAGGAG GAGGATGAAG



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FIG. 7A - Continued

	701		750
hpp32			
AF008216			g
TSU6	a		t
TSU3			g
TSU1	a		t
P8			
P3			
L3			
FT3-3			g
FT3-18			
FT2-4	a		t
FT2-2			g
FT1-7			
FT1-3			
FT1-11	a		t
D5			
D3	a		t
D1			
Consensus	AAGGTTATAA CGATGGAGAG GTAGATGACG AGGAAGATGA AGAAGAGCTT		800
	751		

hpp32			c	
AF008216			t	
TSU6			ta	a
TSU3			t	
TSU1			ta	a
P8			c	
P3			c	
L3			c	
FT3-3			t	
FT3-18			c	
FT2-4			ta	a
FT2-2			t	
FT1-7			c	
FT1-3			c	
FT1-11			ta	a
D5			c	
D3			ta	a
D1			c	
Consensus	GGTGAAAGAAG AAAGGGGTCA GAAGCGAAAA -GAGAACCTG AAGATGAGGG			

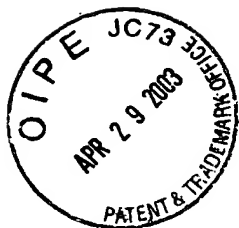


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FIG. 7A - Continued

	850			
801				
hpp32				
AF008216			a	
TSU6	c	c	t	t
TSU3			a	
TSU1	c	c	t	t
P8				
P3				
L3				
FT3-3			a	
FT3-18				
FT2-4	c	c	t	t
FT2-2			a	
FT1-7				
FT1-3				
FT1-11	c	c	t	t
D5				
D3	c	c	t	
D1				
Consensus	AGAAGATGAT	GACTAAGTGG	AATAACCTAT	TTTGAAAAAT TCCTATTGTG

	851				900			
hpp32								
AF008216					a	c
TSU6	t		g	g	c	...	a	
TSU3						...		
TSU1	t		g	g		...	a	
P8								
P3								
L3								
FT3-3					a	...		
FT3-18			g	g		...	a	
FT2-4	t		g	g		...	a	
FT2-2					c	...		
FT1-7								
FT1-3								
FT1-11	t		g	g		...	a	
D5								
D3								
D1								
Consensus	ATTTGACTGT	TTTTACCCAT	ATCCCCTCTC	CCCCCCCCCT	CTAATCCTGC			

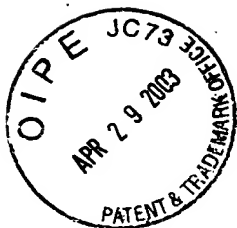


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FIG. 7A - Continued

901

hpb32	(SEQ ID NO: 8)
AF008216	(SEQ ID NO: 9)
TSU6	(SEQ ID NO: 10)
TSU3	(SEQ ID NO: 11)
TSU1	(SEQ ID NO: 12)
P8	(SEQ ID NO: 13)
P3	(SEQ ID NO: 14)
L3	(SEQ ID NO: 15)
FT3-3	(SEQ ID NO: 16)
FT3-18	(SEQ ID NO: 17)
FT2-4	(SEQ ID NO: 18)
FT2-2	(SEQ ID NO: 19)
FT1-7	(SEQ ID NO: 20)
FT1-3	(SEQ ID NO: 21)
FT1-11	(SEQ ID NO: 22)
D5	(SEQ ID NO: 23)
D3	(SEQ ID NO: 24)
D1	(SEQ ID NO: 25)
Consensus CCCCTGAA	(SEQ ID NO: 7)



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50

1

hnp32								
TSU-6			g					l n
TSU-1	kw			f	q			
PC3-8								l n
PC3-3	kw			f	q			k
FT3-3		s	a	a		a		l n
FT3-18	kw			f	q			k
FT2-2		s	a			a		
FT1-7								
DU-145-5								
DU-145-3								
Consensus								

MEMGRRIHLE LRNRTPSDVK ELVLDNSRSN EGKLEGLTDE FEELEFLSTI

100

51

hnp32								
TSU-6								
TSU-1	i							
PC3-8								
PC3-3	i							
FT3-3	g	sd	.	r	...			t y
FT3-18	i					a v		
FT2-2	g	sd	.	r	...k			t y
FT1-7			.	r	...			t y
DU-145-5								t
DU-145-3								
Consensus								

NVGLTSIANL PKLNKLKKLE LSSNRVSGGL EVLAEKCPNL IHLNLSGNKI

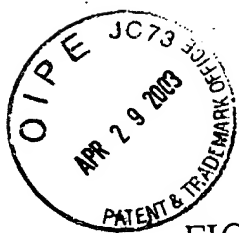
150

101

hnp32								
TSU-6			e	t	n			
TSU-1			e	t	n			
PC3-8				s				
PC3-3			e	t	n			
FT3-3		q				g	l	scyw
FT3-18			e	t	n			
FT2-2		q				g	l	scyw
FT1-7		q				g	l	scyw
DU-145-5								
DU-145-3								
Consensus								

KDLSTIEPLK ELENLKSLDL FNCEVTNLND YRENVFKLLP QLTYLDGYDR

FIG. 7B



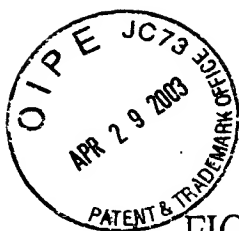
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FIG. 7B - Continued

	151					200
hpp32	-----					
TSU-6	-----					
TSU-1	-----					
PC3-8						
PC3-3						
FT3-3	h y i dh		g h		g e	
FT3-18	-----		-----		-----	
FT2-2	h y i dh		g h		g e	
FT1-7	h y i dh		g h		g eg	
DU-145-5	-----		-----		-----	
DU-145-3	-----		-----		-----	
Consensus	EDKEAPDSDA	EGYVEGLDDE	EEDEDEEEYD	EDAQVVEDEE	DEDEEEEEGEE	
	201					249
hpp32	-----					
TSU-6	-----					
TSU-1	-----					
PC3-8						
PC3-3						
FT3-3	gdg		g		-----	
FT3-18	-----		-----		-----	
FT2-2	gd		g		-----	
FT1-7	gd					
DU-145-5	-----		-----		-----	
DU-145-3	-----		-----		-----	
Consensus	EDVSGEEEEED	EEGYNDGEVD	DEEDEEELGE	EERGQKRKRE	PEDEGEDDD	
	1					50
hpp32						
TSU-6		g				l n
TSU-1	kw		f	q		
PC3-8						l n
PC3-3	kw		f	q		k
FT3-3	s	a	a		a	l n
FT3-18	kw		f	q		k
FT2-2	s	a			a	
FT1-7						
DU-145-5			v			
DU-145-3						
Consensus	MEMGRIHLE	LRNRTPSDVK	ELVLDNSRSN	EGKLEGLTDE	FEELEFLSTI	

FIG. 7B - Continued

	51			d		t	100
hpp32							
TSU-6				a v			
TSU-1	i			a v			
PC3-8				a v			
PC3-3	i			a v			
FT3-3	g	sd	. r	...		t y	
FT3-18	i			a v			
FT2-2	g	sd	. r	...k		t y	
FT1-7			. r	...		t y	
DU-145-5				d		t	
DU-145-3				d			
Consensus	NVGLTSIANL	PKLNKLKKLE	LSSNRVSGGL	EVLAEKCPNL	IHLNLSGNKI		
	101						150
hpp32			e	t	n	-----	-----
TSU-6			e	t	n	-----	-----
TSU-1				s			
PC3-8			e	t	n		
PC3-3							
FT3-3		q				g l	scyw
FT3-18			e	t	n	-----	-----
FT2-2		q				g l	scyw
FT1-7		q				g l	scyw
DU-145-5							
DU-145-3			e	t	n	-----	-----
Consensus	KDLSTIEPLK	KLENLKSLDL	FNCEVTNLND	YRENVFKLLP	QLTYLDGYDR		
	151						200
hpp32							
TSU-6	-----	-----	-----	-----	-----	-----	-----
TSU-1	-----	-----	-----	-----	-----	-----	-----
PC3-8							
PC3-3							
FT3-3	h	y i	dh	g h		g e	
FT3-18	-----	-----	-----	-----	-----	-----	-----
FT2-2	h	y i	dh	g h		g e	
FT1-7	h	y i	dh	g h		g eg	
DU-145-5							
DU-145-3	-----	-----	-----	-----	-----	-----	-----
Consensus	DDKEAPSDA	EGYVEGLDDE	EEDDEEEYYD	EDAQVVEDEE	DEDEEEEEGEE		



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FIG. 7B - Continued

	201		249
hpp32			(SEQ ID NO: 27)
TSU-6	-----	-----	(SEQ ID NO: 28)
TSU-1	-----	-----	(SEQ ID NO: 29)
PC3-8			(SEQ ID NO: 30)
PC3-3			(SEQ ID NO: 31)
FT3-3	gdg	g	(SEQ ID NO: 32)
FT3-18	-----	-----	(SEQ ID NO: 33)
FT2-2	gd	g	(SEQ ID NO: 34)
FT1-7	gd		(SEQ ID NO: 35)
DU-145-5			(SEQ ID NO: 36)
DU-145-3	-----	-----	(SEQ ID NO: 37)
Consensus	EDVSGEEEEED	EEGYNDGEVD	DEEDEEELGE EERGQKRKRE PEDEGEDDD (SEQ ID NO: 26)